A computational framework for particle and whole cell tracking applied to a real biological dataset

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Objectives

The human fibrosarcoma cell line HT-1080 obtained from DSMZ, Germany

Outline

F. Yang, C. Venkataraman, V. Styles, V. Kuttenberger, E. Horn, Z. von Guttenberg, A. Madzvamuse, Journal of Biomechanics,

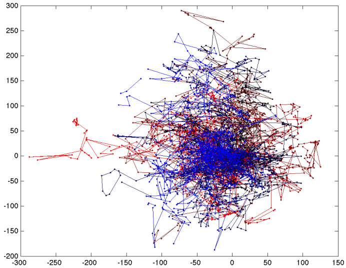
Accepted for publication, http://dx.doi.org/10.1016/j.jbiomech.2016.02.008, 2016.

- Identification from phase contrast microscopy
- Particle tracking
- Whole cell tracking for morphological changes
  - Optimal control of phase field formulations of geometric evolution laws
  - Efficient solver
  - Applications

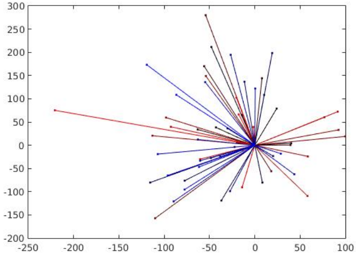
Techniques based upon background removal

Directions of migration

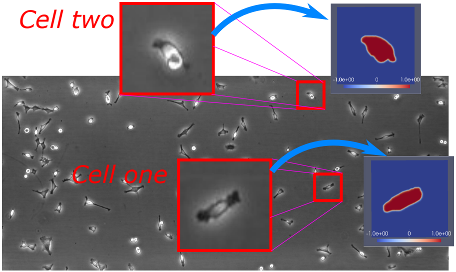
Spider plot

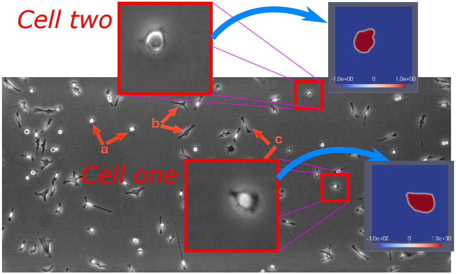


Star plot



Individual cells





Our optimal control model

The mass constrained mean curvature flow with forcing:

$$\begin{cases} \boldsymbol{V}(\boldsymbol{x},t) & = (-\sigma H(\boldsymbol{x},t) + \eta(\boldsymbol{x},t) + \lambda_V(t))\, \boldsymbol{v}(\boldsymbol{x},t) \text{ on } \Gamma(t), t \in (0,T], \\ \Gamma(0) = \Gamma^0. \end{cases}$$

The phase-field approximation of the above equation - Allen-Cahn:

$$\begin{cases} \partial_t \phi(\boldsymbol{x},t) & = \triangle \phi(\boldsymbol{x},t) - \frac{1}{\epsilon^2} G'(\phi(\boldsymbol{x},t)) - \frac{1}{\epsilon}(\eta(\boldsymbol{x},t) - \lambda(t)) \text{ in } \Omega \times (0,T], \\ \nabla \phi \cdot \boldsymbol{\nu}_\Omega & = 0 \text{ on } \partial\Omega \times (0,T], \\ \phi(\cdot,0) & = \phi^0 \text{ in } \Omega. \end{cases}$$

Our optimal control model cont.

The objective functional:

$$J(\phi,\eta) = \frac{1}{2}\int_{\Omega}\left(\phi(\boldsymbol{x},T) - \phi_{obs}(\boldsymbol{x})\right)^2 d\boldsymbol{x} + \frac{\theta}{2}\int_0^T\int_{\Omega}\eta(\boldsymbol{x},t)^2 d\boldsymbol{x}dt,$$

and now we solve the minimisation problem:

$$min_{\eta} J(\phi,\eta), \text{ with } J \text{ given above.}$$

Our optimal control model cont.

The adjoint equation to help computing the derivative of the objective functional:

$$\begin{cases} \partial_t p(\boldsymbol{x}, t) = -\triangle p(\boldsymbol{x}, t) + \epsilon^{-2} G''\left(\phi\left(\boldsymbol{x}, t\right)\right) p(\boldsymbol{x}, t) & \text{in } \Omega \times [0, T), \\ p(\boldsymbol{x}, T) = \phi(\boldsymbol{x}, T) - \phi_{obs}(\boldsymbol{x}) & \text{in } \Omega, \end{cases}$$

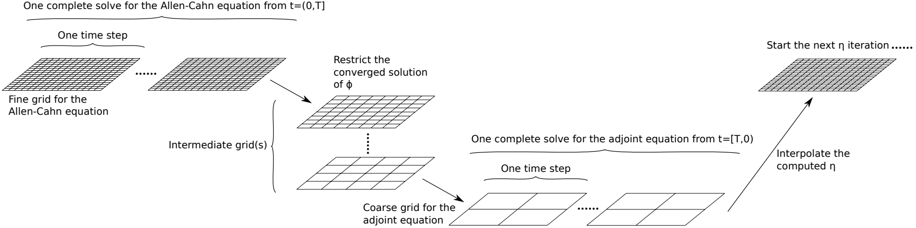
and we update the control as

$$\eta^{\ell+1} = \eta^{\ell} - \alpha\left(\theta\eta^{\ell} + \frac{1}{\epsilon} p^{\ell}\right).$$

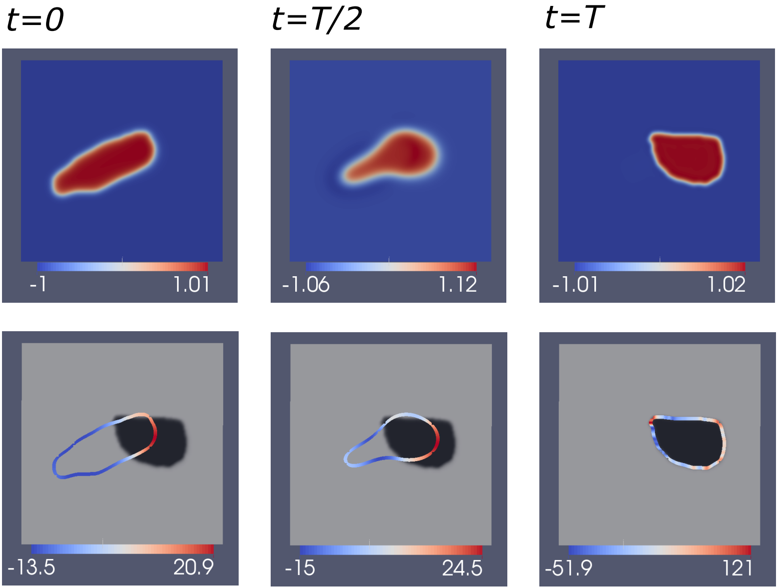
Numerical challenges

- Number of time steps
- Memory requirement (let's consider double precision and 100 time steps)
    - 2-D: 512^2 requires 0.4 gigabytes
    - 3-D: 512^3 requires 215 gigabytes

Two-grid solution strategy



Cell one

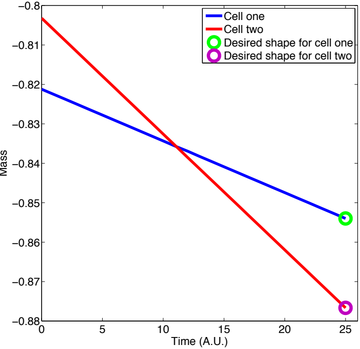


Cell one video

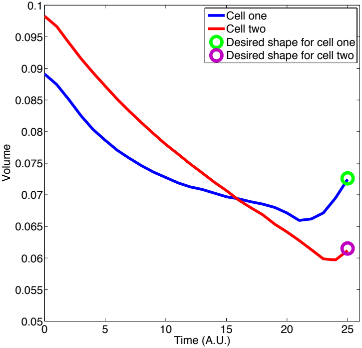
Cell two video

Analysis through tracking morphological changes

$\int_\Omega \phi d\boldsymbol{x}$



$\int_{\{\phi>0\}} 1 d\boldsymbol{x}$



Real world example (2)

Euler number for topological changes

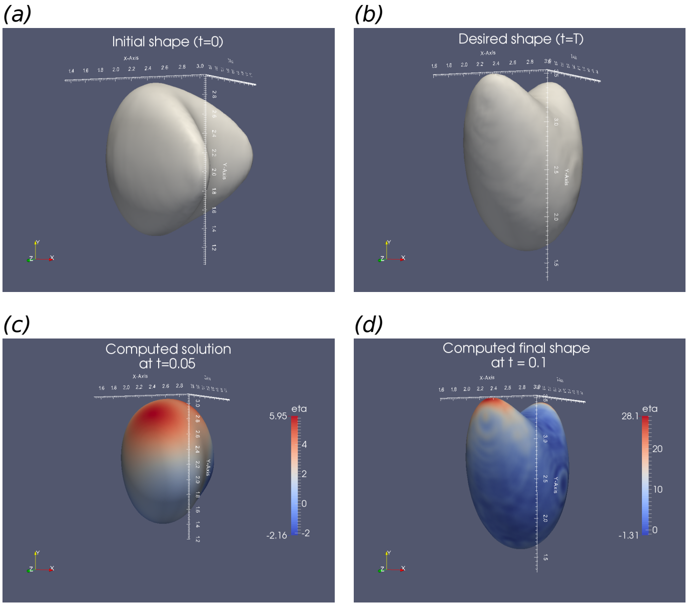
We compute this Euler number for these time steps with an "optimized" control η:

$$\mathcal{X} = \frac{1}{2\pi(a-b)} \int_{\Omega(a,b)} \left(-\triangle\phi + \frac{\nabla|\nabla\phi|^2 \cdot \nabla\phi}{2|\nabla\phi|^2} \right) dx.$$

Q. Du et al. *J. Appl. Math.*, 2005

Real world example (2)

A 3-D example


(a)
Initial shape (t=0)
X-Axis
Y-Axis
(b)
Desired shape (t=T)
X-Axis
Y-Axis
(c)
Computed solution
at t=0.05
X-Axis
Y-Axis
eta
5.95
4
2
0
-2
-2.16
(d)
Computed final shape
at t = 0.1
X-Axis
Y-Axis
eta
28.1
20
10
0
-1.31

A 3-D example video

The end

F.W. Yang, C.E. Goodyer, M.E. Hubbard and P.K. Jimack

"An Optimally Efficient Technique for the Solution of Systems of Nonlinear Parabolic Partial Differential Equations"

AiES in review, 2015

F. Yang, C. Venkataraman, V. Styles and A. Madzvamuse

"A Robust and Efficient Adaptive Multigrid Solver for the Optimal Control of Phase Field Formulations of Geometric Evolution Laws"

CiCP in review, 2015

F. Yang, C. Venkataraman, V. Styles, V.Kuttenberger, E. Horn, Z.von Guttenberg and A. Madzvamuse

"A Computational Framework for Particle and Whole Cell Tracking Applied to a Real Biological Dataset"

JBM Accepted for publication, http://dx.doi.org/10.1016/j.jbiomech.2016.02.008, 2016.